

STIC-Biotech/ChemLib

102555

From: Chen, Shin-Lin
Sent: Wednesday, August 27, 2003 7:17 PM
To: STIC-Biotech/ChemLib
Subject: sequence search: 09/865,018

Please perform the following **sequence search** for Application No. **09/865,018** ASAP. Thanks!

SEQ ID NOs. 1 and 2.

Shin-Lin Chen
AU 1632
CM1 12A15
Mail Box: CM1 12E12
(703) 305-1678

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

The first part of the document discusses the importance of maintaining accurate records of all transactions. It emphasizes that proper record-keeping is essential for the success of any business and for the protection of the interests of all parties involved. The document then goes on to describe the various methods and procedures that should be followed in order to ensure the accuracy and reliability of the records. It also discusses the importance of regularly reviewing and updating the records to reflect any changes in the business or in the law.

The second part of the document discusses the importance of maintaining accurate records of all transactions. It emphasizes that proper record-keeping is essential for the success of any business and for the protection of the interests of all parties involved. The document then goes on to describe the various methods and procedures that should be followed in order to ensure the accuracy and reliability of the records. It also discusses the importance of regularly reviewing and updating the records to reflect any changes in the business or in the law.

The third part of the document discusses the importance of maintaining accurate records of all transactions. It emphasizes that proper record-keeping is essential for the success of any business and for the protection of the interests of all parties involved. The document then goes on to describe the various methods and procedures that should be followed in order to ensure the accuracy and reliability of the records. It also discusses the importance of regularly reviewing and updating the records to reflect any changes in the business or in the law.

The fourth part of the document discusses the importance of maintaining accurate records of all transactions. It emphasizes that proper record-keeping is essential for the success of any business and for the protection of the interests of all parties involved. The document then goes on to describe the various methods and procedures that should be followed in order to ensure the accuracy and reliability of the records. It also discusses the importance of regularly reviewing and updating the records to reflect any changes in the business or in the law.

The fifth part of the document discusses the importance of maintaining accurate records of all transactions. It emphasizes that proper record-keeping is essential for the success of any business and for the protection of the interests of all parties involved. The document then goes on to describe the various methods and procedures that should be followed in order to ensure the accuracy and reliability of the records. It also discusses the importance of regularly reviewing and updating the records to reflect any changes in the business or in the law.



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number:

TO: Shin-Lin Chen
Location: CM1/12A15/12E12
Art Unit: 1632
Tuesday, September 02, 2003

Case Serial Number: 09865018

From: Mary Jane Ruhl
Location: Biotech-Chem Library
CM1-6A06
Phone: 605-1155

maryjane.ruhl@uspto.gov

Search Notes

Examiner Chen,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
CM-1, Rm. 6-A-06
605-1155

10

11

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run #6 August 29, 2003, 15:25:11, Search time 2600 seconds

(without alignments)
9343480 Million cell updates/sec

Title: US-09-865-018B-1

Perfect score: 597
Sequence: 1 atgtcaaaagtgtgagtgatgtc tttgagagagatgtgagagttat 597

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 2889711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 577422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_bai: *
2: gb_htg: *
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Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	597	100.0	597	AR057188	AR057188 Sequence
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11	592.8	97.5	2340	AF247551	AF247551 Homo sapi
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25	591	99.0	1420	BD080718	BD080718 Inhibitor
26	589.1	98.7	1121	BD080724	BD080724 Inhibitor
27	587.8	98.5	1121	AR219449	AR219449 Sequence
28	587.8	98.5	1121	AR282513	AR282513 Sequence
29	582	97.5	582	BD080945	BD080945 Method to
30	523.4	87.7	948	DB4649	DB4649 Fetus virus
31	518.6	86.9	1327	AR031957	AR031957 Sus scrofa
32	518.6	86.9	1301	AR031956	AR031956 Sus scrofa
33	518.6	86.9	1301	AR031955	AR031955 Sus scrofa
34	518.6	86.9	1301	BD017675	BD017675 Nucleic acid
35	499.4	83.7	557	AR219452	AR219452 Sequence
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45	498.4	83.5	1073	AR282517	AR282517 Sequence

ALIGNMENTS

RESULT 1
AR000109
LOCUS AR000109 597 bp DNA linear PAT 04-039-1948
DEFINITION Sequence from patent US 5736418.
ACCESSION AR000109
VERSION AR000109.1 GI:4962640
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 597)
AUTHORS Munger K. and Jones D. Leanne.
TITLE Method and kit for evaluating human papillomavirus trans- and cells
JOURNAL Patent: US 5736418-A 3 07-ATR-1998;

[illegible][illegible]

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RESULT 8	
LOCUS	HSU10906
DEFINITION	Human cyclin-dependent kinase inhibitor p27kip1 mRNA, complete cds
ACCESSION	M10906
VERSION	U10906.1 GI:516558
KEYWORDS	
SOURCE	Homo sapiens (human)

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1 (bases 1 to 597)	Poljak, K., Lee, Mong, -Hong., Edjument-Breomage, H., Koffi, A., Roberts, I. M., Tempst, P. and Massague, J.	Cloning of p27kip1, a cyclin-dependent kinase inhibitor, and a potential mediator of extracellular anti-mitogenic signals	Cell 78, 56-66 (1994)	2 (bases 1 to 597)

JOURNAL
Submitted (15-JUN-1994) M -R [ae and T Missavage, Cell Biology and
Genetics, Memorial Sloan-Kettering Cancer Center, 1275 York Avenue,
New York, NY 10021, USA
FEATURES
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Location/Qualifiers
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Db	61	GCGGAGACACCCCAAGGCGCTTGGGCTTCAGAGAACTCTTGGGCGGCTGGAGCACTAAATAG	120
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QY	181	AATTCGATTTTACGAATCAAAATCTCTTACAGAGCAATATTAAGTGGTAAATATCTTAG	240
Db	181	AATTCGATTTTACGAATCAAAATCTCTTACAGAGCAATATTAAGTGGTAAATATCTTAG	240
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Db	301	GTATGCTGCTTGGGCAATCTATCTAGATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	360

QY	361	GCTGTGGCTAAAC	CTGGAGGACACACG	ATTGGTGGACGACG	ATGATCTGCTGGACACG	420
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QY <td>361</td> <td>GTCTGGGCTAAC <td>CTGGAGGACACG <td>ATTGGTGGACGACG <td>ATGATCTGCTGGACACG <td>420</td> </td></td></td></td>	361	GTCTGGGCTAAC <td>CTGGAGGACACG <td>ATTGGTGGACGACG <td>ATGATCTGCTGGACACG <td>420</td> </td></td></td>	CTGGAGGACACG <td>ATTGGTGGACGACG <td>ATGATCTGCTGGACACG <td>420</td> </td></td>	ATTGGTGGACGACG <td>ATGATCTGCTGGACACG <td>420</td> </td>	ATGATCTGCTGGACACG <td>420</td>	420
QY <td>421</td> <td>CAATCGGGCTAAC <td>GGGACACG <td>ATTGGTGGACGACG <td>ATGATCTGCTGGACACG <td>480</td> </td></td></td></td>	421	CAATCGGGCTAAC <td>GGGACACG <td>ATTGGTGGACGACG <td>ATGATCTGCTGGACACG <td>480</td> </td></td></td>	GGGACACG <td>ATTGGTGGACGACG <td>ATGATCTGCTGGACACG <td>480</td> </td></td>	ATTGGTGGACGACG <td>ATGATCTGCTGGACACG <td>480</td> </td>	ATGATCTGCTGGACACG <td>480</td>	480
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QY <td>421</td> <td>CAATCGGGCTAAC <td>GGGACACG <td>ATTGGTGGACGACG <td>ATGATCTGCTGGACACG <td>480</td> </td></td></td></td>	421	CAATCGGGCTAAC <td>GGGACACG <td>ATTGGTGGACGACG <td>ATGATCTGCTGGACACG <td>480</td> </td></td></td>	GGGACACG <td>ATTGGTGGACGACG <td>ATGATCTGCTGGACACG <td>480</td> </td></td>	ATTGGTGGACGACG <td>ATGATCTGCTGGACACG <td>480</td> </td>	ATGATCTGCTGGACACG <td>480</td>	480

[illegible]

DEFINITION	home sapiens cyclin-dependent kinase inhibitor 27kDp1 mRNA, complete cds.
ACCESSION	AF247551
VERSION	AF247551.1
KEYWORDS	GI:7769664

[illegible]

REFERENCE
AUTHORS
TITLE
JOURNAL
2 (Pages 1 to 597)
Li J, Wang W-L, Yang X-K, and Yu X-X.
Direct Submission
Submitted (22 MAR 2009) Department, Fourth Military Medical
University, No. 17 Changle West Rd., Xi'an, Shaanxi 710042, P. R.
China
FEATURES
Source
Location/Qualifiers
1. 597
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Covered Match	90-79	Score	96-42	Top %	80-77
Host Local Stim	90-99	prevd %	70-100		
Matchups	5962	Constructive	12	Misadvice	02

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DEFINITION	Human samples, similar to cytotrophoblast & placental in (Fig. 2)
ACCESSION	KIP13, c10000, M675304 IMAGE: 440441, mRNA, complete cds
VERSION	W001971.1 (1:128050)4
KEYWORDS	Human, cytotrophoblast (trophoblast)

REFERENCE
 EKKARAYOT, M., LIZON, C., HEDDICH, C., VANDEL, V., CHATELAIN, A., BOUTEVILLE, A.,
 MUMFORD, J., FATHALLAH, P., MATHOS, C., VAILLANT, B., BOUMELAL, H., and
 1. (October 1 to 2, 1994)
REFERENCE
 STRAUSSER, L. R.
 Direct Substitution
 Submitted to J. JAN. 2000. Features and factors of the *in situ* polymerization
 of methyl methacrylate in the presence of a radical scavenger.

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 "OUT OF THE BOX" 100% 100% 100% 100% 100%

model, cytoskeletal attachment, and cytoskeleton reorganization. Arch Biochem Biophys 440:1–10 (2006).

RNA library preparation: <http://bioinformatics.jhu.edu/~liu/seqprep/>.

RNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305. Web site: <http://www.sbs.stanford.edu>

Statistical (Cytoscape, Mark) model: <http://standards.stanford.edu>

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Received 12 November 2006; Accepted 12 December 2006

Features

- **Comprehensive Product Information:** Detailed descriptions, specifications, and pricing for all products.
- **User-Friendly Navigation:** Easy-to-use search and filtering options to find products quickly.
- **Secure Checkout Process:** Streamlined and safe transaction flow.
- **Customer Support:** Accessible assistance channels for inquiries and issues.
- **Mobile Responsiveness:** Optimized viewing and purchasing experience on smartphones and tablets.
- **Personalized Recommendations:** Tailored suggestions based on user browsing history and preferences.
- **Robust Security Measures:** Implementation of SSL encryption and secure payment gateways to protect user data and transactions.
- **Integration Capabilities:** Seamless connection with external systems like inventory management and shipping services.
- **Analytics and Reporting:** Tools to track sales performance, user behavior, and website effectiveness.
- **Scalability:** Architecture designed to handle increasing product volume and user traffic.
- **Compliance Adherence:** Ensuring the platform meets relevant legal and industry standards.

[illegible]

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      1708      /product = Simul (0, 'yr' in dependent_kinase_reaction, the
      1709      /product in (0, 'AH01971.1')
      1710      /dls, 81+1, 0.21, 1, 200, 0.15, 0

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BASE CATALYST	60°C	65°C	70°C
None	0.00	0.00	0.00
NaOH	0.00	0.00	0.00
KOH	0.00	0.00	0.00
LiOH	0.00	0.00	0.00
Ca(OH) ₂	0.00	0.00	0.00
Mg(OH) ₂	0.00	0.00	0.00
Zn(OH) ₂	0.00	0.00	0.00
Al(OH) ₃	0.00	0.00	0.00
Fe(OH) ₃	0.00	0.00	0.00
Cu(OH) ₂	0.00	0.00	0.00
Ni(OH) ₂	0.00	0.00	0.00
Co(OH) ₂	0.00	0.00	0.00
Mn(OH) ₂	0.00	0.00	0.00
Pb(OH) ₂	0.00	0.00	0.00
Ba(OH) ₂	0.00	0.00	0.00
Strontium hydroxide	0.00	0.00	0.00
Ammonium hydroxide	0.00	0.00	0.00
Sodium acetate	0.00	0.00	0.00
Potassium acetate	0.00	0.00	0.00
Lithium acetate	0.00	0.00	0.00
Calcium acetate	0.00	0.00	0.00
Magnesium acetate	0.00	0.00	0.00
Zinc acetate	0.00	0.00	0.00
Aluminum acetate	0.00	0.00	0.00
Iron(III) acetate	0.00	0.00	0.00
Copper(II) acetate	0.00	0.00	0.00
Nickel(II) acetate	0.00	0.00	0.00
Cobalt(II) acetate	0.00	0.00	0.00
Manganese(II) acetate	0.00	0.00	0.00
Lead(II) acetate	0.00	0.00	0.00
Barium acetate	0.00	0.00	0.00
Strontium acetate	0.00	0.00	0.00
Ammonium acetate	0.00	0.00	0.00
Sodium formate	0.00	0.00	0.00
Potassium formate	0.00	0.00	0.00
Lithium formate	0.00	0.00	0.00
Calcium formate	0.00	0.00	0.00
Magnesium formate	0.00	0.00	0.00
Zinc formate	0.00	0.00	0.00
Aluminum formate	0.00	0.00	0.00
Iron(III) formate	0.00	0.00	0.00
Copper(II) formate	0.00	0.00	0.00
Nickel(II) formate	0.00	0.00	0.00
Cobalt(II) formate	0.00	0.00	0.00
Manganese(II) formate	0.00	0.00	0.00
Lead(II) formate	0.00	0.00	0.00
Barium formate	0.00	0.00	0.00
Strontium formate	0.00	0.00	0.00
Ammonium formate	0.00	0.00	0.00
Sodium oxalate	0.00	0.00	0.00
Potassium oxalate	0.00	0.00	0.00
Lithium oxalate	0.00	0.00	0.00
Calcium oxalate	0.00	0.00	0.00
Magnesium oxalate	0.00	0.00	0.00
Zinc oxalate	0.00	0.00	0.00
Aluminum oxalate	0.00	0.00	0.00
Iron(III) oxalate	0.00	0.00	0.00
Copper(II) oxalate	0.00	0.00	0.00
Nickel(II) oxalate	0.00	0.00	0.00
Cobalt(II) oxalate	0.00	0.00	0.00
Manganese(II) oxalate	0.00	0.00	0.00
Lead(II) oxalate	0.00	0.00	0.00
Barium oxalate	0.00	0.00	0.00
Strontium oxalate	0.00	0.00	0.00
Ammonium oxalate	0.00	0.00	0.00
Sodium succinate	0.00	0.00	0.00
Potassium succinate	0.00	0.00	0.00
Lithium succinate	0.00	0.00	0.00
Calcium succinate	0.00	0.00	0.00
Magnesium succinate	0.00	0.00	0.00
Zinc succinate	0.00	0.00	0.00
Aluminum succinate	0.00	0.00	0.00
Iron(III) succinate	0.00	0.00	0.00
Copper(II) succinate	0.00	0.00	0.00
Nickel(II) succinate	0.00	0.00	0.00
Cobalt(II) succinate	0.00	0.00	0.00
Manganese(II) succinate	0.00	0.00	0.00
Lead(II) succinate	0.00	0.00	0.00
Barium succinate	0.00	0.00	0.00
Strontium succinate	0.00	0.00	0.00
Ammonium succinate	0.00	0.00	0.00
Sodium malonate	0.00	0.00	0.00
Potassium malonate	0.00	0.00	0.00
Lithium malonate			

[illegible][illegible][illegible][illegible][illegible]

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GenCore Version 5.1.6
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OM nucleic acid search, using SW model

Run on August 29, 2003, 16:07:16 Search time 62 Seconds

(without alignments)
4250 092 Million cell updates/sec

Title: US-09-865-018B-1

Perfect score: 597

Sequence: 1 atgtcaaacgtgcgagtc

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Search: 56978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 119976

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_NA*
1: /cgn2_6/ptodata/2/lna/5A.COMB.seq*
2: /cgn2_6/ptodata/2/lna/5B.COMB.seq*
3: /cgn2_6/ptodata/2/lna/6A.COMB.seq*
4: /cgn2_6/ptodata/2/lna/6B.COMB.seq*
5: /cgn2_6/ptodata/2/lna/PTNUS.COMB.seq*
6: /cgn2_6/ptodata/2/lna/backfiles.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597	100.0	597	US-08-406-248-3	Sequence 1, Appl
2	597	100.0	597	US-08-897-333A-1	Sequence 1, Appl
3	597	100.0	597	US-09-240-906-6	Sequence 5, Appl
4	597	100.0	597	US-08-794-002-1	Sequence 1, Appl
5	597	100.0	597	US-09-457-568-25	Sequence 25, Appl
6	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
7	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
8	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
9	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
10	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
11	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
12	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
13	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
14	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
15	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
16	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
17	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
18	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
19	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
20	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
21	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
22	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
23	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
24	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
25	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
26	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
27	597	100.0	597	US-09-457-646-25	Sequence 25, Appl

28	499.4	83.7	597	US-09-516-065-11	Sequence 11, Appl
29	498.5	83.5	1028	US-09-457-646-15	Sequence 15, Appl
30	498.6	83.5	1028	US-09-457-646-15	Sequence 15, Appl
31	498.6	83.5	1028	US-08-902-572-21	Sequence 21, Appl
32	498.6	83.5	1028	US-09-516-065-15	Sequence 15, Appl
33	498.4	83.5	1073	US-09-457-646-13	Sequence 13, Appl
34	498.4	83.5	1073	US-09-457-646-13	Sequence 13, Appl
35	498.4	83.5	1073	US-09-516-065-13	Sequence 13, Appl
36	498.4	83.5	1073	US-09-516-065-13	Sequence 13, Appl
37	498.4	83.5	1073	US-08-854-0398-3	Sequence 3, Appl
38	467.6	78.3	594	US-09-240-906-7	Sequence 7, Appl
39	467.6	78.3	594	US-08-794-002-3	Sequence 3, Appl
40	447.6	75.0	534	US-08-794-002-5	Sequence 5, Appl
41	447.6	75.0	534	US-08-854-0398-5	Sequence 5, Appl
42	213.2	35.7	972	US-09-457-646-29	Sequence 29, Appl
43	213.2	35.7	972	US-09-516-065-29	Sequence 29, Appl
44	212.6	35.6	782	US-09-457-646-21	Sequence 21, Appl
45	212.6	35.6	782	US-09-457-646-21	Sequence 21, Appl

ATTACHMENTS

RESULT 1
US-08-406-248-3
Sequence 3, Application US/08406248
Patent No. 5736318
GENERAL INFORMATION:
APPLICANT: Munger, Karl
TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ann Louise Kerner, Ph.D., Leffin & Kerner
STREET: 200 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
AFFIDAVIT NUMBER: US-08-248-348
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Melnikovs, Tatiana A.
REGISTRATION NUMBER: 77194
REFERENCE/SEQUENCE NUMBER: EAC-011
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ. ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Adult
TISSUE TYPE: Kidney
IMMEDIATE SOURCE:
CLONE: p27k1p1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..597
PUBLICATION INFORMATION:

PRIOR APPLICATION NUMBER: 60/128 515
 PRIOR FILING DATE: 1999-04-09
 PRIOR APPLICATION NUMBER: 60/128,271
 PRIOR FILING DATE: 1999-04-08
 PRIOR APPLICATION NUMBER: 60/122,974
 PRIOR FILING DATE: 1999-03-01
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 25
 LENGTH: 597
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-516-065-25

Query Match 100.0% Score 597; DB 4; Length 597;
 Best Local Similarity 100.0% Freq. No. 2 6 170.
 Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGTCACAACTGTCAGAGTCTAAGCGAGAGCCCTAGGCGAGCGATGAGCGCCAGCGAG 60
 1 AATGTCACAACTGTCAGAGTCTAAGCGAGAGCCCTAGGCGAGCGATGAGCGCCAGCGAG 60
 61 GCGAG 120
 61 GCGAG 120
 121 TTAATCGAGTCTGAG 180
 121 TTAATCGAGTCTGAG 180
 181 AATTCGATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAG 240
 181 AATTCGATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAG 240
 241 AAGGCGAGCTGCGCGAGCTTACTACAGAGCCCGCGCGCGCGCGCGCGCGCGCGCGAG 300
 241 AAGGCGAGCTGCGCGAGCTTACTACAGAGCCCGCGCGCGCGCGCGCGCGCGCGCGAG 300
 301 GTGCGGCGAG 360
 301 GTGCGGCGAG 360
 361 GCTCGGCTAAGCTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGA 420
 361 GCTCGGCTAAGCTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGA 420
 421 CAG 480
 421 CAG 480
 481 TCTACTCAAAACAAAG 540
 481 TCTACTCAAAACAAAG 540
 541 GCGAG 597
 541 GCGAG 597

RESULT 8
 US-09-457-568-9
 Sequence 9, Application US/09457568
 Patent No. 6413943
 GENERAL INFORMATION:
 APPLICANT: McArthur, James G
 APPLICANT: Gyuris, Jeno
 APPLICANT: Finer, Mitchell H
 TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
 TITLE REFERENCE: 106482, 691
 CURRENT APPLICATION NUMBER: US/094575, 568
 PRIOR FILING DATE: 1999-12-09
 EARLIER APPLICATION NUMBER: 60/122,974

EARLIER FILING DATE: 1999-03-01
 EARLIER APPLICATION NUMBER: 60/163,682
 EARLIER FILING DATE: 1999-11-05
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 9
 LENGTH: 1098
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-457-568-9

Query Match 99.4% Score 593.4; DB 4; Length 1098;
 Best Local Similarity 99.8% Freq. No. 4 36 169;
 Matches 594; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GTTAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCA 62
 1 GTTAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCA 62
 504 GTTAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCA 563
 504 GTTAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCA 563
 63 GCGAG 122
 63 GCGAG 122
 123 AAGCGGAGCTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCA 182
 123 AAGCGGAGCTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCA 182
 183 TTTGATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCA 242
 183 TTTGATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCA 242
 243 GCGAG 302
 243 GCGAG 302
 303 GCGAG 362
 303 GCGAG 362
 363 TCGGCTAAGCTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCA 422
 363 TCGGCTAAGCTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCAAAATTTTGAAGTCA 422
 423 GCGAG 482
 423 GCGAG 482
 483 TACTCAAAACAAAG 542
 483 TACTCAAAACAAAG 542
 543 GCGAG 597
 543 GCGAG 597
 1044 GCGAG 1098
 1044 GCGAG 1098

RESULT 9
 US-09-457-568-9
 Sequence 9, Application US/09457646
 Patent No. 6420345
 GENERAL INFORMATION:
 APPLICANT: Patel, Satish D
 APPLICANT: McArthur, James G
 APPLICANT: Gyuris, Jeno
 APPLICANT: Finer, Mitchell H
 TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
 TITLE REFERENCE: 106482, 287
 CURRENT APPLICATION NUMBER: US/094575, 646
 PRIOR FILING DATE: 1999-12-09
 EARLIER APPLICATION NUMBER: 60/122,974
 PRIOR FILING DATE: 1999-03-01
 EARLIER APPLICATION NUMBER: 60/163,682
 EARLIER FILING DATE: 1999-11-05


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: Sequence 5, Application US/0951665
: Patent No. 6521602
: GENERAL INFORMATION:
: APPLICANT: Patel, Sall D
: APPLICANT: McArthur, James G
: APPLICANT: Gyuris, Jeno
: APPLICANT: Mendez, Michel
: APPLICANT: Finer, Mitchell
: TITLE OF INVENTION: Anti-Neoplastic Compositions and Uses thereof
: FILE REFERENCE: Col: 409; 106482.692
: CURRENT APPLICATION NUMBER: US/09/516.065
: CURRENT FILING DATE: 2000-03-01
: PRIOR APPLICATION NUMBER: 60/128.515
: PRIOR FILING DATE: 1999-04-09
: PRIOR APPLICATION NUMBER: 60/128.271
: PRIOR FILING DATE: 1999-04-08
: PRIOR APPLICATION NUMBER: 60/122.974
: PRIOR FILING DATE: 1999-03-01
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO: 9
: LENGTH: 1098
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-516-065-9

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Query Match      99.4% Score 593.4: DB 4: Length 1098:
Best Local Similarity 99.8%: Pred No. 4.4e-169:
Matches 594: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 3 GTCAACGTCGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 62
DB 504 GTCAACGTCGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 563
OY 63 GGAAGTACCTGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 122
DB 564 GGAAGTACCTGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 623
OY 123 AACCGGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 182
DB 624 AACCGGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 684
OY 183 TTTCGATTTTGAATATCAAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATG 242
DB 684 TTTCGATTTTGAATATCAAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATG 744
OY 243 GGGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 302
DB 744 GGGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 804
OY 303 GGGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 362
DB 804 GGGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 864
OY 363 TTTCGATTTTGAATATCAAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATG 422
DB 864 TTTCGATTTTGAATATCAAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATG 924
OY 423 GATGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 482
DB 924 GATGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 984
OY 483 TACTCAAAACAAAGAGGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC 542
DB 984 TACTCAAAACAAAGAGGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC 1044
OY 543 CGGTTCTGTGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 597
DB 1044 CGGTTCTGTGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 1098

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: Sequence 7, Application US/9457568
: Patent No. 6413943
: GENERAL INFORMATION:
: APPLICANT: McArthur, James G
: APPLICANT: Gyuris, Jeno
: APPLICANT: Finer, Mitchell H
: TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
: FILE REFERENCE: 106482.691
: CURRENT APPLICATION NUMBER: 60/128.568
: CURRENT FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: 60/122.974
: PRIOR FILING DATE: 1999-03-01
: PRIOR APPLICATION NUMBER: 60/128.682
: PRIOR FILING DATE: 1999-11-05
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO: 7
: LENGTH: 1143
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-457-568-7

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Query Match      99.4% Score 594.4: DB 4: Length 1143:
Best Local Similarity 99.8%: Pred No. 4.4e-169:
Matches 594: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 3 GTCAACGTCGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 62
DB 549 GTCAACGTCGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 608
OY 63 GGAAGTACCTGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 122
DB 609 GGAAGTACCTGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 668
OY 123 AACCGGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 182
DB 669 AACCGGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 728
OY 183 TTTCGATTTTGAATATCAAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATG 242
DB 729 TTTCGATTTTGAATATCAAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATG 788
OY 243 GGGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 302
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OY 303 GGGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 362
DB 849 GGGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 908
OY 363 TTTCGATTTTGAATATCAAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATG 422
DB 909 TTTCGATTTTGAATATCAAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATG 968
OY 423 GATGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 482
DB 969 GATGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 1028
OY 483 TACTCAAAACAAAGAGGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC 542
DB 1029 TACTCAAAACAAAGAGGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC 1088
OY 543 CGGTTCTGTGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 597
DB 1089 CGGTTCTGTGAGTGTCTTAACGGAGCCCTAGCCGTGAGCGATGATGAGTAAAGT 1143

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RESULT 12
US-09-457-568-7

RESULT 13
US-09-457-646-7
: Sequence 7, Application US/9457568
: Patent No. 6420345
: GENERAL INFORMATION:

Query Match	75.0%	Score 447.6;	DB 10;	Length 534
Best Local Similarity	89.9%;	Prd	No 1.4e-128	

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Db	139	ATGTGCAACGTGGCAGATGTCTTAAGCGGAGGCGGAAAGGATGATGAGGAGACAG	198		
Oy	61	GGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	140		



GenCore version 5.1.6
Copyright (c) 1993 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 29, 2003, 14:10:31 : Search time 1661 Seconds
(without alignments)
7796.761 Million cell updates/sec

Title: US-09-865-018b-1
Perfect score: 597
Sequence: 1 atgtcaacgctgcagctgc... : ttagagagagctcgaacgctaa 597

Scoring table: IDENTITY-NUC
Gapop 10.0 : Gapext 1.0

Searched: 2278192 seqs, 1152238256 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

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13: qb_est4:*
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29: qb_gss2:*

Prod No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	593.8	99.5	842	9	A0121935 A0121935
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3	582.6	97.6	601	9	A0127449 A0127449
4	579.8	97.1	920	14	BX410337 BX410337

RESULT 1	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	COMMENT
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	Unpublished	Contact: Takao Isegai	
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	Genomics Laboratory	Helix Research Institute	
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	1532-3 Yama, Kisarazu, Chiba 292-0812, Japan	Tel: 81-438-52-3975	
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	1532-3 Yama, Kisarazu, Chiba 292-0812, Japan	Fax: 81-438-52-3986	
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	1532-3 Yama, Kisarazu, Chiba 292-0812, Japan	Email: tisegai@hri.co.jp	
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	1532-3 Yama, Kisarazu, Chiba 292-0812, Japan	HRI Human cDNA project	
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	1532-3 Yama, Kisarazu, Chiba 292-0812, Japan	Research in Human cDNA Library construction Department of	

ALIGNMENTS

RESULT 1	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	COMMENT
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	Unpublished	Contact: Takao Isegai	
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	Genomics Laboratory	Helix Research Institute	
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	1532-3 Yama, Kisarazu, Chiba 292-0812, Japan	Tel: 81-438-52-3975	
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	1532-3 Yama, Kisarazu, Chiba 292-0812, Japan	Fax: 81-438-52-3986	
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	1532-3 Yama, Kisarazu, Chiba 292-0812, Japan	Email: tisegai@hri.co.jp	
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	1532-3 Yama, Kisarazu, Chiba 292-0812, Japan	HRI Human cDNA project	
A0121935	A0121935	1	GI:10937170	EST	Homo sapiens (human)	1532-3 Yama, Kisarazu, Chiba 292-0812, Japan	Research in Human cDNA Library construction Department of	

LOCUS	H0268198	578 bp	mRNA	linear	EST 97-MAY-2000
DEFINITION	U96d02.21 Human insulinoma cDNA clones (cDNA) from IMR39-77C250 5' similar to SW-CDB_HUMAN P46527 CYCLIN-DEPENDENT KINASE INHIBITOR 1B ; mRNA sequence.				
ACCESSION	U96d8188 .1 GI:20493247				
VERSION	1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 578) Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kastner,K., Lemshka,I., Scarse,M., Bresnelli,J., Grawoll,G., Clifton,S., Hallier,L., Marra,M., Page,D., White,T., Martin,J., Bislain,A., Schmitt,A., Theising,B., Rutter,E., Fong,O.T., Bennett,T., Caldas, S.M., Gibbons,M., McCann,P., Cole,P., Tsagarelis,W.L., Williams,T., Jackson,Y., and Bowers,Y. Endocrine Pancreas Consortium Unpublished Other ESTs: U96d02.x1 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@molcp.harvard.edu Library was constructed by Dr T. Ferrer in vivo mass-selected plasmid SK- by Dr. H. Inoue DNA sequencing by Washington University Genome Sequencing Center for information on obtaining a clone please contact Dr. Hiroshi Inoue (hinoue@wustl.edu) Seq primer: -40RP from Gibco High quality sequence stop: 429. Location/Qualifiers 1..578 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5779250" /tissue_type="insulinoma" /lab_host="DH10B (phage-resistant)" /clone_lib="Human Insulinoma" /note="(Organ pancreas): Vector: phagescript SK, Site:1 XhoI; Site:2: EcoRI; Constructed with lambda ZAPI system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to plasmid SK- by Dr. H. Inoue following the Washington University protocol (http://genome.wustl.edu/rest/lambdaprotocol.shtml). Please contact Hiroshi Inoue, MD/PhD for further information on this library (Medadiolam Division, Endocrinology Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave., St. Louis, MO 63110) Note: This is a Washington University Pancreas EST project library."				
BASE COUNT	151 a 152 c 188 g 87 t				
ORIGIN					
Query Match	86.2% Score 514.4, DP 13 Length 578				
Best Local Similarity	99.8%; Pred No. 8 2e+10;				
Matches 515;	Conservative 0; Mismatch 1; Indels 0; Gaps 0				
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DB					
OY	63 ATGTCAACGCGGCAGTCTGAACGGATACCGTAATCATCTGATGATGAGATGACATTCAGCCAG 122				
DB					
OY	121 TTAACTCGGAGATTGAGAGAGATCTGATGATAATGAAGAAGAGAGAGAGAGAGAGAGAGAGAG 180				
DB					
OY	183 TTAATCGGAGATTGAGAGAGATCTGATGATAATGAAGAAGAGAGAGAGAGAGAGAGAGAGAG 242				
DB					

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3y      241  AAGGCGAATCTTGCGGCCACTTCTCACTATCAATAGCAGGCGCGCGCGCGCGCGCGCGCGCG 300
        |||||||
4y      303  AAGCGCACAGCTGTGGCGCGAGTCTCACTACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 362
        |||||||
5y      401  GTTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
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6y      363  GTCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 422
        |||||||
7y      421  CAGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
        |||||||
8y      423  GTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 482
        |||||||
9y      421  CAGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
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Db      483  CAGACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 542
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Dd      543  TCTACTCAAAACAAAAGAGCCACAGCAAGCAAGCAAGCAA 578
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RESULT 7
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LOCUS     EMBL1101104
DEFINITION Homo sapiens HBB gene; protein: Hemoglobin beta, mRNA
sequence.
Accession A0117363
Version   A0117363.1
Keywords  EST.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens (human)
KEYWORDS  Homo sapiens
REFERENCE 1 (bases 1 to 783)
AUTHORS  Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,I., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isono,T.
TITLE     HRI human cDNA project
JOURNAL   Unpublished
COMMENT   Contact: Yukio Isozaki
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          HRI human cDNA project; 5' & 3'-end and core-pass sequencing; Helix
          Research Institute; cDNA library construction; Department of
          Virology, Institute of Medical Science, University of Tokyo, and
          Helix Research Institute.
FEATURES
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